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Sequence Listing was accepted.

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Reviewer: Saleem, Syed (ASRC)

Timestamp: [year=2010; month=8; day=2; hr=12; min=15; sec=29; ms=352;]

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Application No: 10535341

Version No: 2.1

Input Set:

Output Set:

Started: 2010-08-02 12:13:53.463

Finished: 2010-08-02 12:13:55.362

Elapsed: 0 hr(s) 0 min(s) 1 sec(s) 899 ms

Total Warnings: 9

Total Errors: 0

No. of SeqIDs Defined: 26

Actual SeqID Count: 26

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (1)
W 213	Artificial or Unknown found in <213> in SEQ ID (2)
W 213	Artificial or Unknown found in <213> in SEQ ID (6)
W 213	Artificial or Unknown found in <213> in SEQ ID (7)
W 213	Artificial or Unknown found in <213> in SEQ ID (11)
W 213	Artificial or Unknown found in <213> in SEQ ID (12)
W 213	Artificial or Unknown found in <213> in SEQ ID (16)
W 213	Artificial or Unknown found in <213> in SEQ ID (19)
W 213	Artificial or Unknown found in <213> in SEQ ID (20)

SEQUENCE LISTING

<110> HANMI PHARM. IND. CO., LTD.
 <120> IgG Fc FRAGMENT FOR A DRUG CARRIER AND METHOD FOR THE PREPARATION THEREOF
 <130> Q115525
 <140> 10535341
 <141> 2006-06-09

<150> PCT/KR04/02942
 <151> 2004-11-13

<150> KR 10-2003-0080299
 <151> 2003-11-13

<160> 26

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<210> 1
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 <213> Artificial Sequence

<220>
 <223> primer

<400> 1
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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer

<400> 2
 ggggggatcct catttaccba gagacaggga gaggtctctt tg 42

<210> 3
 <211> 12
 <212> PRT
 <213> Homo sapiens

<400> 3
 Glu Ser Lys Tyr Gly Pro Pro Cys Pro Ser Cys Pro

1 5 10

<210> 4
<211> 663
<212> DNA
<213> homo sapiens

<400> 4
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aaggacactc tcatgatctc ccggaccctt gaggtcacgt gcgtgggtgt ggacgtgagc 120
caggaagacc ccgaggtcca gttcaactgg tacgtggatg gcgtggaggt gcataatgcc 180
aagacaaagc cgcggggagga gcagttcaac agcacgtacc gtgtgggtcag cgtcctcacc 240
gtcctgcacc aggactggct gaacggcaag gagtacaagt gcaaggcttc caacaaaggc 300
ctcccgctct ccatcgagaa aaccatctcc aaagccaaag ggcagccccg agagccacag 360
gtgtacaccc tgcccccatc ccaggaggag atgaccaaga accagggtcag cctgacctgc 420
ctggtcaaag gcttctaccc cagcgacatc gccgtggagt gggagagcaa tgggcagccg 480
gagaacaact acaagaccac gcctcccggt ctggactccg acggctcctt ctctctctac 540
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tga 663

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<211> 69
<212> DNA
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gccagggcg 69

<210> 6
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 6
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<210> 7
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 7
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<210> 8
<211> 220
<212> PRT
<213> homo sapiens

<400> 8
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1 5 10 15

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
20 25 30

Thr Cys Val Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe
35 40 45

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
50 55 60

Arg Glu Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
65 70 75 80

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
85 90 95

Ser Asn Lys Gly Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala
100 105 110

Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln
115 120 125

Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
130 135 140

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
145 150 155 160

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
165 170 175

Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu
180 185 190

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His

195

200

205

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
 210 215 220

<210> 9
 <211> 654
 <212> DNA
 <213> homo sapiens

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 cccgaggtcc agttcaactg gtacgtggat ggcgtggagg tgcataatgc caagacaaag 180
 ccgcgggagg agcagttcaa cagcacgtac cgtgtggtca gcgtcctcac cgtcctgcac 240
 caggactggc tgaacggcaa ggagtacaag tgcaaggtct ccaacaaagg cctcccgtcc 300
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 ctgcccccat cccaggagga gatgaccaag aaccagggtca gcctgacctg cctggtcaaa 420
 ggcttctacc ccagcgacat cgccgtggag tgggagagca atgggcagcc ggagaacaac 480
 tacaagacca cgctcccgt gctggactcc gacggctcct tcttctcta cagcaggcta 540
 accgtggaca agagcaggtg gcaggagggg aatgtcttct catgctccgt gatgcatgag 600
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<210> 10
 <211> 217
 <212> PRT
 <213> homo sapiens

<400> 10
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 1 5 10 15
 Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
 20 25 30
 Val Val Asp Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr
 35 40 45
 Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
 50 55 60
 Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
 65 70 75 80
 Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys

85					90					95						
Gly	Leu	Pro	Ser	Ser	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	
100					105					110						
Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Gln	Glu	Glu	Met	
115					120					125						
Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	
130					135					140						
Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	
145					150					155					160	
Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	
165					170					175						
Tyr	Ser	Arg	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Glu	Gly	Asn	Val	
180					185					190						
Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	
195					200					205						
Lys	Ser	Leu	Ser	Leu	Ser	Leu	Gly	Lys								
210					215											

<210> 11
 <211> 33
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer

<400> 11
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<210> 12
 <211> 33
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer

<400> 12
 gggggatcct catttaccg gagacaggga gag 33

<210> 13
 <211> 15
 <212> PRT
 <213> homo sapiens

<400> 13
 Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro
 1 5 10 15

<210> 14
 <211> 660
 <212> DNA
 <213> homo sapiens

<400> 14
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 cacgaagacc ctgaggtcaa gttcaactgg tacgtggacg gcgtggaggt gcataatgcc 180
 aagacaaagc cgcgggagga gcagtacaac agcacgtacc gtgtggtcag cgtcctcacc 240
 gtcctgcacc aggactggct gaatggcaag gagtacaagt gcaaggtctc caacaaagcc 300
 ctcccagccc ccacgcagaa aaccatctcc aaagccaaag ggcagccccg agagccacag 360
 gtgtacaccc tgccccatc ccgggatgag ctgaccaaga accaggtcag cctgacctgc 420
 ctggtcaaag gcttctatcc cagcgacatc gccgtggagt gggagagcaa tgggcagccg 480
 gagaacaact acaagaccac gcctcccgtg ctggactccg acggctcctt cttcctctac 540
 agcaagctca ccgtggacaa gagcaggtgg cagcagggga acgtcttctc atgctccgtg 600
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<210> 15
 <211> 220
 <212> PRT
 <213> homo sapiens

<400> 15
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 Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
 20 25 30
 Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
 35 40 45
 Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
 50 55 60
 Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
 65 70 75 80

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
85 90 95

Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
100 105 110

Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg
115 120 125

Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
130 135 140

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
145 150 155 160

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
165 170 175

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
180 185 190

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
195 200 205

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
210 215 220

<210> 16
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 16
cggcacctga actcctgggg ggaccg 26

<210> 17
<211> 651
<212> DNA
<213> homo sapiens

<400> 17
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cctgaggtca agttcaactg gtacgtggac ggcgtggagg tgcataatgc caagacaaag 180
ccgcgggagg agcagtacaa cagcacgtac cgtgtggtca gcgtcctcac cgtcctgcac 240
caggactggc tgaatggcaa ggagtacaag tgcaaggtct ccaacaaagc cctcccagcc 300

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cccatcgaga aaaccatctc caaagccaaa gggcagcccc gagagccaca ggtgtacacc 360
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ggctttctatc ccagcgacat cgccgtggag tgggagagca atgggcagcc ggagaacaac 480
tacaagacca cgcttcccgt gctggactcc gacggtectt tcttcctcta cagcaagctc 540
accgtggaca agagcagggtg gcagcagggg aacgttttct catgctccgt gatgcatgag 600
gctctgcaca accactacac gcagaagagc ctctccctgt ctccgggtaa a 651

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<210>      18
<211>      217
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<213>      homo sapiens

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Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
      20              25              30

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
      35              40              45

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
      50              55              60

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
      65              70              75              80

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
      85              90              95

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
      100              105              110

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
      115              120              125

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
      130              135              140

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
      145              150              155              160

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
      165              170              175

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
      180              185              190

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
      195              200              205

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Lys Ser Leu Ser Leu Ser Pro Gly Lys
210 215

<210> 19
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 19
cgccgtgccc agcacctccg gtggcggga 29

<210> 20
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 20
gggggatcct catttaccgc gagacaggga gag 33

<210> 21
<211> 12
<212> PRT
<213> homo sapiens

<400> 21
Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro
1 5 10

<210> 22
<211> 657
<212> PRT
<213> homo sapiens

<400> 22
Cys Cys Gly Thr Gly Cys Cys Cys Ala Gly Cys Ala Cys Cys Thr Cys
1 5 10 15

Cys Gly Gly Thr Gly Gly Cys Gly Gly Gly Ala Cys Cys Gly Thr Cys
20 25 30

Ala Gly Thr Cys Thr Thr Cys Cys Thr Cys Thr Thr Cys Cys Cys Cys
35 40 45

Cys Cys Ala Ala Ala Ala Cys Cys Cys Ala Ala Gly Gly Ala Cys Ala

50		55		60
Cys Cys Cys Thr Cys Ala Thr Gly Ala Thr Cys Thr Cys Cys Cys Gly				
65		70		75 80
Gly Ala Cys Cys Cys Cys Thr Gly Ala Gly Gly Thr Cys Ala Cys Ala				
	85		90	95
Thr Gly Cys Gly Thr Gly Gly Thr Gly Gly Thr Gly Gly Ala Cys Gly				
	100		105	110
Thr Gly Ala Gly Cys Cys Ala Cys Gly Ala Ala Gly Ala Cys Cys Cys				
	115		120	125
Thr Gly Ala Gly Gly Thr Cys Cys Ala Gly Thr Thr Cys Ala Ala Cys				
	130		135	140
Thr Gly Gly Thr Ala Cys Gly Thr Gly Gly Ala Cys Gly Gly Cys Gly				
145		150		155 160
Thr Gly Gly Ala Gly Gly Thr Gly Cys Ala Thr Ala Ala Thr Gly Cys				
	165		170	175
Cys Ala Ala Gly Ala Cys Ala Ala Ala Gly Cys Cys Gly Cys Gly Gly				
	180		185	190
Gly Ala Gly Gly Ala Gly Cys Ala Gly Thr Thr Thr Ala Ala Cys Ala				
	195		200	205
Gly Cys Ala Cys Gly Thr Thr Thr Cys Gly Thr Gly Thr Gly Gly Thr				
	210		215	220
Cys Ala Gly Cys Gly Thr Cys Cys Thr Cys Ala Cys Cys Gly Thr Cys				
225		230		235 240
Gly Thr Gly Cys Ala Cys Cys Ala Gly Gly Ala Cys Thr Gly Gly Cys				
	245		250	255
Thr Gly Ala Ala Thr Gly Gly Cys Ala Ala Gly Gly Ala Gly Thr Ala				
	260		265	270
Cys Ala Ala Gly Thr Gly Cys Cys Ala Ala Gly Gly Thr Cys Thr Cys Cys				
	275		280	285
Ala Ala Cys Ala Ala Ala Gly Gly Cys Cys Thr Cys Cys Cys Ala Gly				
	290		295	300
Cys Cys Cys Cys Cys Ala Thr Cys Gly Ala Gly Ala Ala Ala Ala Cys				
305		310		315 320
Cys Ala Thr Cys Thr Cys Cys Ala Ala Ala Ala Cys Cys Ala Ala Ala				
	325		330	335
Gly Gly Gly Cys Ala Gly Cys Cys Cys Cys Gly Ala Gly Ala Gly Cys				
	340		345	350
Cys Ala Cys Ala Gly Gly Thr Gly Thr Ala Cys Ala Cys Cys Cys Thr				

355

360

365

Gly Cys Cys Cys Cys Cys Ala Thr Cys Cys Cys Gly Gly Gly Ala Ala
370 375 380

Gly Ala Gly Ala Thr Gly Ala Cys Cys Ala Ala Gly Ala Ala Cys Cys
385 390 395 400

Ala Gly Gly Thr Cys Ala Gly Cys Cys Thr Gly Ala Cys Cys Thr Gly
405 410 415

Cys Cys Thr Gly Gly Thr Cys Ala Ala Ala Gly Gly Cys Thr Thr Cys
420 425 430

Thr Ala Thr Cys Cys Cys Ala Gly Cys Gly Ala Cys Ala Thr Cys Gly
435 440 445

Cys Cys Gly Thr Gly Gly Ala Gly Thr Gly Gly Gly Ala Gly Ala Gly
450 455 460

Cys Ala Ala Thr Gly Gly Gly Cys Ala Gly Cys Cys Gly Gly Ala Gly
465 470 475 480

Ala Ala Cys Ala Ala Cys Thr Ala Cys Ala Ala Gly Ala Cys Cys Ala
485 490 495

Cys Gly Cys Cys Thr